



0590
0405

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/016,516
Source: OTPE
Date Processed by STIC: 4/11/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/016,816

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☒ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/016,516

DATE: 04/11/2002

TIME: 13:20:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Houtzager, Erwin
4 Vijn, Irma Maria Caecilia
5 Sijmons, Peter Christiaan
7 <120> TITLE OF INVENTION: A Structure for Presenting Desired Peptide Sequences
9 <130> FILE REFERENCE: 2183-5208US
11 <140> CURRENT APPLICATION NUMBER: US 10/016,516
12 <141> CURRENT FILING DATE: 2001-12-10
E--> 14 <160> NUMBER OF SEQ ID NOS: 17/18 (P.24)
16 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
19 <211> LENGTH: 291
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' end of exemplary
maximal
25 primary scaffold.
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <222> LOCATION: (79)..(93)
30 <223> OTHER INFORMATION: The nucleotide at each of positions 79-93 may be any
nucleotide.
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <222> LOCATION: (157)..(159)
35 <223> OTHER INFORMATION: The nucleotide at each of positions 157-159 may be any
nucleotide.
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: (214)..(222)
40 <223> OTHER INFORMATION: The nucleotide at each of positions 214-222 may be any
nucleotide.
42 <400> SEQUENCE: 1
E--> 43 aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa
44 aac gat gac gat ctt 54
47 Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
W--> 48 Asp Leu
W--> 49
E--> 50 10 15
E--> 52 aag ctc acg tgc cgt gct gaa ggt nnn nnn nnn nnn nnn

(GLOBAL ERRORS) See Error Summary Sheet, item 1

53 tac tgc atg ggt tgg 108
W--> 55 Lys Leu Thr Cys Arg Ala Glu Gly Xaa Xaa Xaa Xaa Xaa Tyr Cys Met
W--> 56 Gly Trp

same env

RAW SEQUENCE LISTING

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

W--> 57 20
E--> 58 25 30 35
E--> 60 ttc cgt cag gcg ccg aac gac gac agt act aac gtg gcc
W--> 61 acg atc tta nnn ggg 162
63 Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Leu
W--> 64 Xaa Gly
W--> 65 40 45
E--> 66 50
E--> 68 agc acg tac tac ggt gac tcc gtc aaa gag cgc ttc gat
W--> 69 atc cgt cgc gac nnn 216
71 Ser Thr Tyr Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile Arg Arg
W--> 72 Asp Xaa
W--> 73 55 60
E--> 74 65 70
E--> 76 nnn nnn aac acc gtt acc tta tcg atg gac gat ctg caa
77 ccg gaa gac tct gca 270
W--> 79 Xaa Xaa Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro Glu Asp
W--> 80 Ser Ala
W--> 81 75
E--> 82 80 85 90
E--> 85 gaa tac aat tgt gca ggt tct
86 291
88 Glu Tyr Asn Cys Ala Gly Ser
W--> 89 95
91 <210> SEQ ID NO: 2
92 <211> LENGTH: 42
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' end of exemplary
maximal
98 primary scaffold.
100 <400> SEQUENCE: 2
E--> 102 tac cac tac cgt ggt cag ggt acc gac gtt acc gtc tcg
103 tcg 42
105 Tyr His Tyr Arg Gly Gln Gly Thr Asp Val Thr Val Ser Ser
W--> 106 1 5 10
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 405
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Description of Artificial Sequence: Scaffold with VHH 1MEL
CDR
117 regions.
119 <400> SEQUENCE: 3
E--> 120 aat gtg aaa ctg gtt gaa aaa ggt ggc aat ttc gtc gaa
121 aac gat gac gat ctt 54
123 Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
W--> 124 Asp Leu
W--> 125 1 5

RAW SEQUENCE LISTING

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

same

```

E--> 126 10          15
E--> 128 aag  ctc  acg  tgc  cgt  gct  gaa  ggt  tac  acc  att  ggc  ccg
      129 tac  tgc  atg  ggt  tgg          108
      131 Lys  Leu  Thr  Cys  Arg  Ala  Glu  Gly  Tyr  Thr  Ile  Gly  Pro  Tyr  Cys  Met
W--> 132 Gly  Trp
W--> 133
E--> 134 25          30          35          20
E--> 136 ttc  cgt  cag  gcg  ccg  aac  gac  gac  agt  act  aac  gtg  gcc
      137 acg  atc  aac  atg  ggt          162
      139 Phe  Arg  Gln  Ala  Pro  Asn  Asp  Asp  Ser  Thr  Asn  Val  Ala  Thr  Ile  Asn
W--> 140 Met  Gly
W--> 141
E--> 142 50
E--> 144 ggc  ggt  att  acg  tac  tac  ggt  gac  tcc  gtc  aaa  gag  cgc
      145 ttc  gat  atc  cgt  cgc          216
      147 Gly  Gly  Ile  Thr  Tyr  Tyr  Gly  Asp  Ser  Val  Lys  Glu  Arg  Phe  Asp  Ile
W--> 148 Arg  Arg
W--> 149
E--> 150 65          70          55          60
E--> 152 gac  aac  gcg  tcc  aac  acc  gtt  acc  tta  tcg  atg  gac  gat
      153 ctg  caa  ccg  gaa  gac          270
      155 Asp  Asn  Ala  Ser  Asn  Thr  Val  Thr  Leu  Ser  Met  Asp  Asp  Leu  Gln  Pro
W--> 156 Glu  Asp
W--> 157
E--> 158 80          85          90          75
E--> 160 tct  gca  gaa  tac  aat  tgt  gca  ggt  gat  tct  acc  att  tac
      161 gcg  agc  tat  tat  gaa          324
      163 Ser  Ala  Glu  Tyr  Asn  Cys  Ala  Gly  Asp  Ser  Thr  Ile  Tyr  Ala  Ser  Tyr
W--> 164 Tyr  Glu
W--> 165
E--> 166 100        105          95
E--> 168 tgt  ggt  cat  ggc  ctg  agt  acc  ggc  ggt  tac  ggc  tac  gat
      169 agc  cac  tac  cgt  ggt          378
      171 Cys  Gly  His  Gly  Leu  Ser  Thr  Gly  Gly  Tyr  Gly  Tyr  Asp  Ser  His  Tyr
W--> 172 Arg  Gly
W--> 173
E--> 174 115        120          125          110
E--> 177 cag  ggt  acc  gac  gtt  acc  gtc  tcg  tcg
      178 405
      180 Gln  Gly  Thr  Asp  Val  Thr  Val  Ser  Ser
W--> 181
      183 <210> SEQ ID NO: 4
      184 <211> LENGTH: 422
      185 <212> TYPE: DNA
      186 <213> ORGANISM: Artificial Sequence
      188 <220> FEATURE:
      189 <223> OTHER INFORMATION: Description of Artificial Sequence: Scaffold with VHH 1BZQ
CDR
      190 regions.
      192 <400> SEQUENCE: 4

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RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/016,516

TIME: 13:20:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

same

```

E--> 193 aat  gtg  aaa  ctg  gtt  gaa  aaa  ggt  ggc  aat  ttc  gtc  gaa
      194 aac  gat  gac  gat  ctt          54
      196 Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
W--> 197 Asp Leu
W--> 198
E--> 199 10          15          1          5
E--> 201 aag  ctc  acg  tgc  cgt  gct  agc  ggt  tac  gcc  tac  acg  tat
      202 atc  tac  atg  ggt  tgg          108
      204 Lys Leu Thr Cys Arg Ala Ser Gly Tyr Ala Tyr Thr Tyr Ile Tyr Met
W--> 205 Gly Trp
W--> 206
E--> 207 25          30          35          20
E--> 209 ttc  cgt  cag  gcg  ccg  aac  gac  gac  agt  act  aac  gtg  gcc
      210 acc  atc  gac  tcg  ggt          162
      212 Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Asp
W--> 213 Ser Gly
W--> 214
E--> 215 50          40          45
E--> 217 ggc  ggc  ggt  acc  ctg  tac  ggt  gac  tcc  gtc  aaa  gag  cgc
      218 ttc  gat  atc  cgt  cgc          216
      220 Gly Gly Gly Thr Leu Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile
W--> 221 Arg Arg
W--> 222
E--> 223 65          70          55          60
E--> 225 gac  aaa  ggc  tcc  aac  acc  gtt  acc  tta  tcg  atg  gac  gat
      226 ctg  caa  ccg  gaa  gac          270
      228 Asp Lys Gly Ser Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro
W--> 229 Glu Asp
W--> 230
E--> 231 80          85          90          75
E--> 233 tct  gca  gaa  tac  aat  tgt  gca  gcg  ggt  ggc  tac  gaa  ctg
      234 cgc  gac  cgc  acc  tac          324
      236 Ser Ala Glu Tyr Asn Cys Ala Ala Gly Gly Tyr Glu Leu Arg Asp Arg
W--> 237 Thr Tyr
W--> 238
E--> 239 100          105          95
E--> 241 ggt  cag  cgt  ggt  cag  ggt  acc  gac  gtt  acc  gtc  tcg  tcg
E--> 242 383
      244 Gly Gln Arg Gly Gln Gly Thr Asp Val Thr Val Ser Ser
W--> 245
E--> 246 120          110          115
      248 <210> SEQ ID NO: 5
      249 <211> LENGTH: 351
      250 <212> TYPE: DNA
      251 <213> ORGANISM: Artificial Sequence
      253 <220> FEATURE:
      254 <223> OTHER INFORMATION: Description of Artificial Sequence: Scaffold with VHH 1HCV
CDR
      255 regions.
      257 <400> SEQUENCE: 5

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RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/016,516

TIME: 13:20:26

Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

same

```

E--> 258 aat  gtg  aaa  ctg  gtt  gaa  aaa  ggt  ggc  aat  ttc  gtc  gaa
      259 aac  gat  gac  gat  ctt          54
      261 Asn Val Lys Leu Val Glu Lys Gly Gly Asn Phe Val Glu Asn Asp Asp
W--> 262 Asp Leu
W--> 263
E--> 264 10          15
E--> 266 aag  ctc  acg  tgc  cgt  gct  gaa  ggt  cgt  acg  ggt  tcg  acc
      267 tac  gat  atg  ggt  tgg          108
      269 Lys Leu Thr Cys Arg Ala Glu Gly Arg Thr Gly Ser Thr Tyr Asp Met
W--> 270 Gly Trp
W--> 271
E--> 272 25          30          35
E--> 274 ttc  cgt  cag  gcg  ccg  aac  gac  gac  agt  act  aac  gtg  gcc
      275 acg  atc  aac  tgg  gat          162
      277 Phe Arg Gln Ala Pro Asn Asp Asp Ser Thr Asn Val Ala Thr Ile Asn
W--> 278 Trp Asp
W--> 279
E--> 280 50
E--> 282 agc  gcc  cgt  acg  tac  tac  ggt  gac  tcc  gtc  aaa  gag  cgc
      283 ttc  gat  atc  cgt  cgc          216
      285 Ser Ala Arg Thr Tyr Tyr Gly Asp Ser Val Lys Glu Arg Phe Asp Ile
W--> 286 Arg Arg
W--> 287
E--> 288 60          65          70
E--> 290 gac  aat  gcc  tcc  aac  acc  gtt  acc  tta  tcg  atg  gac  gat
      291 ctg  caa  ccg  gaa  gac          270
      293 Asp Asn Ala Ser Asn Thr Val Thr Leu Ser Met Asp Asp Leu Gln Pro
W--> 294 Glu Asp
W--> 295
E--> 296 80          85          90
E--> 298 tct  gca  gaa  tac  aat  tgt  gca  ggt  ggt  gaa  ggc  ggc  acc
      299 tgg  gat  agc  cgt  ggt          324
      302 Ser Ala Glu Tyr Asn Cys Ala Gly Gly Glu Gly Gly Thr Trp Asp Ser
W--> 303 Arg Gly
W--> 304
E--> 305 100          105
E--> 308 cag  ggt  acc  gac  gtt  acc  gtc  tcg  tcg
      309 351
      311 Gln Gly Thr Asp Val Thr Val Ser Ser
W--> 312          110          115
      340 <210> SEQ ID NO: 8
      341 <211> LENGTH: 144
      342 <212> TYPE: PRT
      343 <213> ORGANISM: IF2X - Single Domain Camelid Antibody Cab-Ca05
      345 <220> FEATURE:
      346 <221> NAME/KEY: misc_feature
      347 <222> LOCATION: (7)
      348 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
      349 acid residue.

```


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PATENT APPLICATION: US/10/016,516

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351 <220> FEATURE:
 352 <221> NAME/KEY: misc_feature
 353 <222> LOCATION: (10)..(11)
 354 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 10-11 indicate the absence
 of
 355 amino acid residues.
 357 <220> FEATURE:
 358 <221> NAME/KEY: misc_feature
 359 <222> LOCATION: (13)
 360 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
 an amino
 361 acid residue.
 363 <220> FEATURE:
 364 <221> NAME/KEY: misc_feature
 365 <222> LOCATION: (33)..(37)
 366 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-37 indicate the absence
 of
 367 amino acid residues.
 369 <220> FEATURE:
 370 <221> NAME/KEY: misc_feature
 371 <222> LOCATION: (49)
 372 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
 an amino
 373 acid residue.
 375 <220> FEATURE:
 376 <221> NAME/KEY: misc_feature
 377 <222> LOCATION: (54)..(55)
 378 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
 of
 379 amino acid residues.
 381 <220> FEATURE:
 382 <221> NAME/KEY: misc_feature
 383 <222> LOCATION: (65)..(66)
 384 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-66 indicate the absence
 of
 385 amino acid residues.
 387 <220> FEATURE:
 388 <221> NAME/KEY: misc_feature
 389 <222> LOCATION: (68)..(69)
 390 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 68-69 indicate the absence
 of
 391 amino acid residues.
 393 <220> FEATURE:
 394 <221> NAME/KEY: misc_feature
 395 <222> LOCATION: (101)
 396 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
 an
 397 amino acid residue.
 399 <220> FEATURE:
 400 <221> NAME/KEY: misc_feature
 401 <222> LOCATION: (103)
 402 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
 an

403 amino acid residue.
405 <220> FEATURE:
406 <221> NAME/KEY: misc_feature
407 <222> LOCATION: (140)
408 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
an

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Input Set : A:\EP.txt

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409 amino acid residue. *same format error as described on pgs. 1, 3*

411 <400> SEQUENCE: 8

W--> 412 Gln Val Gln Leu Val Glu Xaa Ser Gly Xaa Xaa Gly Xaa Gly Ser Val

E--> 413 Gln Ala

E--> 414

E--> 415 5 10 15 1

W--> 417 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Xaa Xaa

E--> 418 Xaa Xaa

E--> 420 20 25 30 35

W--> 422 Xaa Val Ser Thr Tyr Cys Met Gly Trp Phe Arg Gln Xaa Ala Pro Gly

E--> 423 Lys Xaa

E--> 424

E--> 425 45 50 40

W--> 427 Xaa Glu Arg Glu Gly Val Ala Thr Ile Leu Xaa Xaa Gly Xaa Xaa Gly

E--> 428 Ser Thr

E--> 429

E--> 430 60 65 70 55

432 Tyr Tyr Gly Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Gln Asp Asn

E--> 433 Ala Lys

E--> 435 75 80 85 90

W--> 437 Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Xaa Lys Xaa Pro Glu Asp

E--> 438 Thr Ala

E--> 439

E--> 440 100 105 95

442 Ile Tyr Tyr Cys Ala Gly Ser Thr Val Ala Ser Thr Gly Trp Cys Ser

E--> 443 Arg Leu

E--> 444

E--> 445 115 120 125 110

W--> 447 Arg Pro Tyr Asp Tyr His Tyr Arg Gly Gln Gly Thr Gln Xaa Val Thr

E--> 448 Val Ser

E--> 449

E--> 450 135 140 130

452 <210> SEQ ID NO: 9

453 <211> LENGTH: 144

454 <212> TYPE: PRT

455 <213> ORGANISM: lQD0 - Camelid Heavy Chain Variable Domain

457 <220> FEATURE:

458 <221> NAME/KEY: misc_feature

459 <222> LOCATION: (7)

460 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of

an amino

461 acid residue.

463 <220> FEATURE:

464 <221> NAME/KEY: misc_feature

465 <222> LOCATION: (10)..(11)

466 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 10-11 indicate the absence

of

467 amino acid residues.

469 <220> FEATURE:

470 <221> NAME/KEY: misc_feature

471 <222> LOCATION: (13)

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Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

472 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
473 acid residue.
475 <220> FEATURE:
476 <221> NAME/KEY: misc_feature
477 <222> LOCATION: (33)..(34)
478 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-34 indicate the absence
479 of amino acid residues.
481 <220> FEATURE:
482 <221> NAME/KEY: misc_feature
483 <222> LOCATION: (49)
484 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
485 an amino acid residue.
487 <220> FEATURE:
488 <221> NAME/KEY: misc_feature
489 <222> LOCATION: (54)..(55)
490 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
491 of amino acid residues
493 <220> FEATURE:
494 <221> NAME/KEY: misc_feature
495 <222> LOCATION: (68)..(69)
496 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 68-69 indicate the absence
497 of amino acid residues.
499 <220> FEATURE:
500 <221> NAME/KEY: misc_feature
501 <222> LOCATION: (101)
502 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
503 an amino acid residue.
505 <220> FEATURE:
506 <221> NAME/KEY: misc_feature
507 <222> LOCATION: (103)
508 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
509 an amino acid residue.
511 <220> FEATURE:
512 <221> NAME/KEY: misc_feature
513 <222> LOCATION: (124)..(126)
514 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 124-126 indicate the
515 absence of amino acid residues.
517 <220> FEATURE:
518 <221> NAME/KEY: misc_feature
519 <222> LOCATION: (140)
520 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
521 an amino acid residue.
523 <400> SEQUENCE: 9
W--> 524 Gln Val Gln Leu Gln Glu Xaa Ser Gly Xaa Xaa Gly Xaa Gly Leu Val
E--> 525 Gln Ala
E--> 526 1 5
E--> 527 10 15
W--> 529 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Xaa Xaa
E--> 530 Ala Ser

same error

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E--> 531

E--> 532 25 30 35

W--> 534 Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Xaa Val Pro Gly

E--> 535 Lys Xaa

E--> 537 40 45 50

W--> 539 Xaa Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Xaa Xaa Lys

E--> 540 Glu Thr

E--> 541

E--> 542 60 65 70

544 Trp Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn

E--> 545 Ala Lys

E--> 547 75 80 85 90

W--> 549 Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Xaa Lys Xaa Gly Glu Asp

E--> 550 Thr Ala

E--> 551

E--> 552 100 105

W--> 554 Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Ala Asp Ile Ser Xaa

E--> 555 Xaa Xaa

E--> 557 110 115 120 125

W--> 559 Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Xaa Val Thr

E--> 560 Val Ser

E--> 561

E--> 562 135 140 130

564 <210> SEQ ID NO: 10

565 <211> LENGTH: 144

566 <212> TYPE: PRT

567 <213> ORGANISM: 8FAB - Heavy Chain from Human Iggl

569 <220> FEATURE:

570 <221> NAME/KEY: misc_feature

571 <222> LOCATION: (7)

572 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
573 acid residue.

575 <220> FEATURE:

576 <221> NAME/KEY: misc_feature

577 <222> LOCATION: (10)..(11)

578 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 10-11 indicate the absence
of
579 amino acid residues.

581 <220> FEATURE:

582 <221> NAME/KEY: misc_feature

583 <222> LOCATION: (13)

584 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
585 acid residue.

587 <220> FEATURE:

588 <221> NAME/KEY: misc_feature

589 <222> LOCATION: (33)..(37)

590 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-37 indicate the absence
of
591 amino acid residues.

593 <220> FEATURE:

594 <221> NAME/KEY: misc_feature

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595 <222> LOCATION: (49)
 596 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
 an amino
 597 acid residue.
 599 <220> FEATURE:
 600 <221> NAME/KEY: misc_feature
 601 <222> LOCATION: (54)..(55)
 602 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
 of
 603 amino acid residues.
 605 <220> FEATURE:
 606 <221> NAME/KEY: misc_feature
 607 <222> LOCATION: (65)..(66)
 608 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-66 indicate the absence
 of
 609 amino acid residues.
 611 <220> FEATURE:
 612 <221> NAME/KEY: misc_feature
 613 <222> LOCATION: (101)
 614 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
 an
 615 amino acid residue.
 617 <220> FEATURE:
 618 <221> NAME/KEY: misc_feature
 619 <222> LOCATION: (103)
 620 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
 an
 621 amino acid residue.
 623 <220> FEATURE:
 624 <221> NAME/KEY: misc_feature
 625 <222> LOCATION: (121)..(127)
 626 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 121-127 indicate the
 absence of
 627 amino acid residues.
 629 <220> FEATURE:
 630 <221> NAME/KEY: misc_feature
 631 <222> LOCATION: (140)
 632 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
 an
 633 amino acid residue.
 635 <400> SEQUENCE: 10
 W--> 636 Ala Val Lys Leu Val Gln Xaa Ala Gly Xaa Xaa Gly Xaa Gly Val Val
 E--> 637 Gln Pro
 E--> 638
 E--> 639 10 15
 W--> 641 Gly Arg Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Xaa Xaa
 E--> 642 Xaa Xaa
 E--> 643
 E--> 644 25 30 35
 W--> 646 Xaa Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Xaa Ala Pro Gly
 E--> 647 Lys Xaa
 E--> 648
 E--> 649 45 50 40

W-->	651	Xaa	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Trp	Xaa	Xaa	Tyr	Asn	Gly	Ser
E-->	652	Arg	Thr														
E-->	653												55				60

same

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same

```

E--> 654 65                                70
      656 Tyr  Tyr  Gly  Asp  Ser  Val  Lys  Gly  Arg  Phe  Thr  Ile  Ser  Arg  Asp  Asn
E--> 657 Ser  Lys
E--> 659 75                                80                                85                                90
W--> 661 Arg  Thr  Leu  Tyr  Met  Gln  Met  Asn  Ser  Leu  Xaa  Arg  Xaa  Thr  Glu  Asp
E--> 662 Thr  Alal
E--> 663
E--> 664 100                                105
W--> 666 Val  Tyr  Tyr  Cys  Ala  Arg  Asp  Pro  Asp  Ile  Leu  Thr  Xaa  Xaa  Xaa  Xaa
E--> 667 Xaa  Xaa
E--> 668
E--> 669 115                                120                                125
W--> 671 Xaa  Ala  Phe  Ser  Phe  Asp  Tyr  Trp  Gly  Gln  Gly  Val  Leu  Xaa  Val  Thr
E--> 672 Val  Ser
E--> 673
E--> 674 135                                140                                130
      676 <210> SEQ ID NO: 11
      677 <211> LENGTH: 144
      678 <212> TYPE: PRT
      679 <213> ORGANISM: 1VSC - Human Vcam-1
      681 <220> FEATURE:
      682 <221> NAME/KEY: misc_feature
      683 <222> LOCATION: (1)
      684 <223> OTHER INFORMATION: The 'Xaa' indicator at position 1 indicates the absence of
an amino
      685 acid residue.
      687 <220> FEATURE:
      688 <221> NAME/KEY: misc_feature
      689 <222> LOCATION: (7)
      690 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
      691 acid residue.
      693 <220> FEATURE:
      694 <221> NAME/KEY: misc_feature
      695 <222> LOCATION: (13)
      696 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
      697 acid residue.
      699 <220> FEATURE:
      700 <221> NAME/KEY: misc_feature
      701 <222> LOCATION: (33)..(39)
      702 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-39 indicate the absence
of
      703 amino acid residues.
      706 <220> FEATURE:
      707 <221> NAME/KEY: misc_feature
      708 <222> LOCATION: (49)
      709 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
an amino
      710 acid residue.
      712 <220> FEATURE:
      713 <221> NAME/KEY: misc_feature
      714 <222> LOCATION: (52)..(77)

```


715 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 52-77 indicate the absence
of

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716 amino acid residues.
 718 <220> FEATURE:
 719 <221> NAME/KEY: misc_feature
 720 <222> LOCATION: (89)..(90)
 721 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 89-90 indicate the absence
 of
 722 amino acid residues.
 724 <220> FEATURE:
 725 <221> NAME/KEY: misc_feature
 726 <222> LOCATION: (101)
 727 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
 an
 728 amino acid residue.
 730 <220> FEATURE:
 731 <221> NAME/KEY: misc_feature
 732 <222> LOCATION: (103)
 733 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
 an
 734 amino acid residue.
 736 <220> FEATURE:
 737 <221> NAME/KEY: misc_feature
 738 <222> LOCATION: (118)..(129)
 739 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 118-129 indicate the
 absence of
 740 amino acid residues.
 742 <220> FEATURE:
 743 <221> NAME/KEY: misc_feature
 744 <222> LOCATION: (136)
 745 <223> OTHER INFORMATION: The 'Xaa' indicator at position 136 indicates the absence of
 an
 746 amino acid residue.
 748 <220> FEATURE:
 749 <221> NAME/KEY: misc_feature
 750 <222> LOCATION: (140)
 751 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
 an
 752 amino acid residue.
 754 <400> SEQUENCE: 11

same error

W--> 755	Xaa	Phe	Lys	Ile	Glu	Thr	Xaa	Thr	Pro	Glu	Ser	Arg	Xaa	Tyr	Leu	Ala
E--> 756	Gln	Ile														
E--> 757																
E--> 758	10															
W--> 760	Gly	Asp	Ser	Val	Ser	Leu	Thr	Cys	Ser	Thr	Thr	Gly	Cys	Glu	Xaa	Xaa
E--> 761	Xaa	Xaa														
E--> 762																
E--> 763	25															
W--> 765	Xaa	Xaa	Xaa	Ser	Pro	Phe	Phe	Ser	Trp	Arg	Thr	Gln	Xaa	Ile	Asp	Xaa
E--> 766	Xaa	Xaa														
E--> 767																
E--> 768	50															
W--> 770	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
E--> 771	Xaa	Xaa														
E--> 772																

E--> 773 65

70

same
W--> 775 Xaa Xaa Xaa Xaa Xaa Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly

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E--> 776 Xaa Xaa
 E--> 777
 E--> 778 80 85 90
 W--> 780 Thr Thr Ser Thr Leu Thr Met Asn Pro Val Xaa Ser Xaa Phe Gly Asn
 E--> 781 Glu His
 E--> 782 95
 E--> 783 100 105
 W--> 785 Ser Tyr Leu Cys Thr Ala Thr Cys Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 E--> 786 Xaa Xaa
 E--> 787 110
 E--> 788 115 120 125
 W--> 790 Xaa Xaa Xaa Ser Arg Lys Leu Glu Lys Xaa Gly Ile Gln Xaa Val Glu
 E--> 791 Ile Tyr
 E--> 792 130 135
 E--> 793 140
 900 <210> SEQ ID NO: 13
 901 <211> LENGTH: 144
 902 <212> TYPE: PRT
 903 <213> ORGANISM: 1F97 - Soluble Part of the Junction Adhesion Molecule from a Mouse
 905 <220> FEATURE:
 906 <221> NAME/KEY: misc_feature
 907 <222> LOCATION: (7)
 908 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
 an amino
 909 acid residue.
 911 <220> FEATURE:
 912 <221> NAME/KEY: misc_feature
 913 <222> LOCATION: (11)
 914 <223> OTHER INFORMATION: The 'Xaa' indicator at position 11 indicates the absence of
 an amino
 915 acid residue.
 917 <220> FEATURE:
 918 <221> NAME/KEY: misc_feature
 919 <222> LOCATION: (13)
 920 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
 an amino
 921 acid residue.
 923 <220> FEATURE:
 924 <221> NAME/KEY: misc_feature
 925 <222> LOCATION: (33)..(39)
 926 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-39 indicate the absence
 of
 927 amino acid residues.
 929 <220> FEATURE:
 930 <221> NAME/KEY: misc_feature
 931 <222> LOCATION: (49)
 932 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
 an amino
 933 acid residue
 935 <220> FEATURE:
 936 <221> NAME/KEY: misc_feature
 937 <222> LOCATION: (51)
 938 <223> OTHER INFORMATION: The 'Xaa' indicator at position 51 indicates the absence of

an amino
939

acid residue.

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941 <220> FEATURE:
 942 <221> NAME/KEY: misc_feature
 943 <222> LOCATION: (54)..(55)
 944 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
 of
 945 amino acid residues
 947 <220> FEATURE:
 948 <221> NAME/KEY: misc_feature
 949 <222> LOCATION: (65)..(72)
 950 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-72 indicate the absence
 of
 951 amino acid residues.
 953 <220> FEATURE:
 954 <221> NAME/KEY: misc_feature
 955 <222> LOCATION: (87)..(92)
 956 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 87-92 indicate the absence
 of
 957 amino acid residues.
 959 <220> FEATURE:
 960 <221> NAME/KEY: misc_feature
 961 <222> LOCATION: (101)
 962 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
 an
 963 amino acid residue
 965 <220> FEATURE:
 966 <221> NAME/KEY: misc_feature
 967 <222> LOCATION: (103)
 968 <223> OTHER INFORMATION: The *use apostrophe* *marked* ~~Xaa~~ indicator at position 103 indicates the absence of
 an
 969 amino acid residue.
 971 <220> FEATURE:
 972 <221> NAME/KEY: misc_feature
 973 <222> LOCATION: (121)..(131)
 974 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 121-131 indicate the
 absence of
 975 amino acid residues.
 977 <220> FEATURE:
 978 <221> NAME/KEY: misc_feature
 979 <222> LOCATION: (140)
 980 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
 an
 981 amino acid residue.
 983 <400> SEQUENCE: 13 *same line*

W-->	984	Lys	Gly	Ser	Val	Tyr	Thr	Xaa	Ala	Gln	Ser	Xaa	Asp	Xaa	Val	Gln	Val
E-->	985	Pro	Glu														
E-->	986																
E-->	987	10															
W-->	989	Asn	Glu	Ser	Ile	Lys	Leu	Thr	Cys	Thr	Tyr	Ser	Gly	Phe	Ser	Xaa	Xaa
E-->	990	Xaa	Xaa														
E-->	991																
E-->	992	25															
W-->	993	Xaa	Xaa	Xaa	Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe	Val	Xaa	Gln	Xaa	Gly
E-->	994	Ser	Xaa														

E--> 995

40

45

E--> 996 50

W--> 998 Xaa Thr Thr Ala Leu Val Cys Tyr Asn Ser Xaa Xaa Xaa Xaa Xaa Xaa

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E--> 999 Xaa Xaa
 E--> 1000
 E--> 1001 60 65 70 55
 W--> 1003 Gln Ile Thr Ala Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Xaa Xaa
 E--> 1004 Xaa Xaa
 E--> 1005 75
 E--> 1006 80 85 90
 W--> 1008 Xaa Xaa Ser Gly Ile Thr Phe Ser Ser Val Xaa Thr Xaa Arg Lys Asp
 E--> 1009 Asn Gly
 E--> 1010 95
 E--> 1011 100 105
 W--> 1013 Glu Tyr Thr Cys Met Val Ser Asx Glu Gly Gly Gln Xaa Xaa Xaa Xaa
 E--> 1014 Xaa Xaa
 E--> 1015 110
 E--> 1016 115 120 125
 W--> 1018 Xaa Xaa Xaa Xaa Xaa Asn Tyr Gly Glu Val Ser Ile His Xaa Leu Thr
 E--> 1019 Val Leu
 E--> 1020 130 135
 E--> 1021 140
 1230 <210> SEQ ID NO: 16
 1231 <211> LENGTH: 144
 1232 <212> TYPE: PRT
 1233 <213> ORGANISM: 1IAR - Human Interleukin-4 Receptor Alpha Chain Complex
 1235 <220> FEATURE:
 1236 <221> NAME/KEY: misc_feature
 1237 <222> LOCATION: (7)
 1238 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
 an amino
 1239 acid residue.
 1241 <220> FEATURE:
 1242 <221> NAME/KEY: misc_feature
 1243 <222> LOCATION: (12)..(16)
 1244 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 12-16 indicate the
 absence of
 1245 amino acid residues.
 1247 <220> FEATURE:
 1248 <221> NAME/KEY: misc_feature
 1249 <222> LOCATION: (49)
 1250 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
 an amino
 1251 acid residue.
 1253 <220> FEATURE:
 1254 <221> NAME/KEY: misc_feature
 1255 <222> LOCATION: (54)..(55)
 1256 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the
 absence of
 1257 amino acid residues.
 1259 <220> FEATURE:
 1260 <221> NAME/KEY: misc_feature
 1261 <222> LOCATION: (65)..(90)
 1262 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-90 indicate the
 absence of
 1263 amino acid residues.

1265 <220> FEATURE:

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1266 <221> NAME/KEY: misc_feature
 1267 <222> LOCATION: (101)
 1268 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence
 of an
 1269 amino acid residue.
 1271 <220> FEATURE:
 1272 <221> NAME/KEY: misc_feature
 1273 <222> LOCATION: (122)..(128)
 1274 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 122-128 indicate the
 absence of
 1275 amino acid residues.
 1277 <220> FEATURE:
 1278 <221> NAME/KEY: misc_feature
 1279 <222> LOCATION: (141)
 1280 <223> OTHER INFORMATION: The 'Xaa' indicator at position 141 indicates the absence
 of an
 1281 amino acid residue.
 1285 <400> SEQUENCE: 16 *same error*

W--> 1286	Arg	Ala	Pro	Gly	Asn	Leu	Xaa	Thr	Val	Asn	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	
E--> 1287	Asn	Val															
E--> 1288												1				5	
E--> 1289	10					15											
	1291	Ser	Asp	Thr	Leu	Leu	Leu	Thr	Trp	Ser	Asn	Pro	Tyr	Pro	Pro	Asp	Asn
E--> 1292	Tyr	Leu															
E--> 1293																20	
E--> 1294	25					30					35						
W--> 1296	Tyr	Asn	His	Leu	Thr	Tyr	Ala	Val	Asn	Ile	Ser	Glu	Xaa	Asn	Asp	Pro	
E--> 1297	Ala	Xaa															
E--> 1298																40	
E--> 1299	45					50											
W--> 1301	Xaa	Asp	Glu	Arg	Ile	Tyr	Asn	Val	Thr	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
E--> 1302	Xaa	Xaa															
E--> 1303												55				60	
E--> 1304	65					70											
W--> 1306	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
E--> 1307	Xaa	Xaa															
E--> 1308																75	
E--> 1309	80					85					90						
W--> 1311	Leu	Glu	Pro	Ser	Leu	Arg	Ile	Ala	Ala	Ser	Xaa	Thr	Leu	Lys	Ser	Gly	
E--> 1312	Ile	Ser															
E--> 1313																95	
E--> 1314	100					105											
W--> 1316	Tyr	Arg	Ala	Arg	Val	Arg	Ala	Trp	Ala	Gln	Ala	Tyr	Asn	Xaa	Xaa	Xaa	
E--> 1317	Xaa	Xaa															
E--> 1318																110	
E--> 1319	115					120				125							
W--> 1321	Xaa	Xaa	Thr	Thr	Trp	Ser	Glu	Trp	Ser	Pro	Ser	Thr	Lys	Trp	Xaa	His	
E--> 1322	Asn	Ser															
E--> 1323																130	
E--> 1324	135																
1444	<210>	SEQ ID NO:	18														
1445	<211>	LENGTH:	363														

same error in seq. 17
last sequence in file

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```

1446 <212> TYPE: DNA
C--> 1447 <213> ORGANISM: Artificial
1449 <220> FEATURE:
1450 <221> NAME/KEY: misc_feature
1451 <223> OTHER INFORMATION: Artificial Sequence: Exemplary primary scaffold used to
obtain
1452         optimal secondary
1453         scaffolds.
1455 <220> FEATURE:
1456 <221> NAME/KEY: misc_feature
1457 <222> LOCATION: (73)..(99)
1458 <223> OTHER INFORMATION: The nucleotide at positions 73-99 may be any nucleotide.
1460 <220> FEATURE:
1461 <221> NAME/KEY: misc_feature
1462 <222> LOCATION: (157)..(177)
1463 <223> OTHER INFORMATION: The nucleotide at positions 157-177 may be any nucleotide.
1465 <220> FEATURE:
1466 <221> NAME/KEY: misc_feature
1467 <222> LOCATION: (292)..(333)
1468 <223> OTHER INFORMATION: The nucleotide at positions 292-333 may be any nucleotide
1470 <400> SEQUENCE: 18
E--> 1472 aat  gtg  aaa  ctg  gtt  gaa  aaa  ggt  ggc  aat  ttc  gtc  gaa
1473 aac  gat  gac  gat  ctt          54
1475 Asn  Val  Lys  Leu  Val  Glu  Lys  Gly  Gly  Asn  Phe  Val  Glu  Asn  Asp  Asp
W--> 1476 Asp  Leu
W--> 1477
E--> 1478 10
E--> 1480 aag  ctc  acg  tgc  cgt  gct  nnn  nnn  nnn  nnn  nnn  nnn  nnn  nnn
W--> 1481 nnn  atg  ggt  tgg 108
W--> 1483 Lys  Leu  Thr  Cys  Arg  Ala  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Met
W--> 1484 Gly  Trp
W--> 1485
E--> 1486 25
E--> 1488 ttc  cgt  cag  gcg  ccg  aac  gac  gac  agt  act  aac  gtg  gcc
W--> 1489 acc  atc  gac  nnn  nnn  162
1491 Phe  Arg  Gln  Ala  Pro  Asn  Asp  Asp  Ser  Thr  Asn  Val  Ala  Thr  Ile  Asp
W--> 1492 Xaa  Xaa
W--> 1493
E--> 1494 50
E--> 1496 nnn  nnn  nnn  nnn  nnn  tac  ggt  gac  tcc  gtc  aaa  gag  cgc
1497 ttc  gat  atc  cgt  cgc  216
W--> 1499 Xaa  Xaa  Xaa  Xaa  Xaa  Tyr  Gly  Asp  Ser  Val  Lys  Glu  Arg  Phe  Asp  Ile
W--> 1500 Arg  Arg
W--> 1501
E--> 1502 60
E--> 1504 gac  aaa  ggc  tcc  aac  acc  gtt  acc  tta  tcg  atg  gac  gat
1505 ctg  caa  ccg  gaa  gac  270
1507 Asp  Lys  Gly  Ser  Asn  Thr  Val  Thr  Leu  Ser  Met  Asp  Asp  Leu  Gln  Pro
W--> 1508 Glu  Asp
W--> 1509

```

same error

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```

E--> 1510 80          85          90
E--> 1512 tct    gca    gaa    tac    aat    tgt    gca    nnn    nnn    nnn    nnn    nnn    nnn
W--> 1513 nnn    nnn    nnn    nnn    nnn    324
W--> 1515 Ser    Ala    Glu    Tyr    Asn    Cys    Ala    Xaa    Xaa    Xaa    Xaa    Xaa    Xaa    Xaa    Xaa
W--> 1516 Xaa    Xaa
W--> 1517
E--> 1518 100      105
E--> 1521 nnn    nnn    nnn    ggt    cag    ggt    acc    gac    gtt    acc    gtc    tcg    tcg
      1522 363
W--> 1524 Xaa    Xaa    Xaa    Gly    Gln    Gly    Thr    Asp    Val    Thr    Val    Ser    Ser
W--> 1525
E--> 1526 120      110      115

```

same

FYI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 04/11/2002

PATENT APPLICATION: US/10/016,516

TIME: 13:20:27

Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

L:43 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:2
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:3
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:254 Repeated in SeqNo=3
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:193 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:4
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
M:254 Repeated in SeqNo=4
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4

VERIFICATION SUMMARY

DATE: 04/11/2002

PATENT APPLICATION: US/10/016,516

TIME: 13:20:27

Input Set : A:\EP.txt

Output Set: N:\CRF3\04112002\J016516.raw

L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:246 M:252 E: No. of Seq. differs, <211>LENGTH:Input:422 Found:363 SEQ:4
 L:258 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:5
 L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 M:254 Repeated in SeqNo=5
 L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:413 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
 M:332 Repeated in SeqNo=8
 L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:525 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
 M:332 Repeated in SeqNo=9
 L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:637 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
 M:332 Repeated in SeqNo=10
 L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
 L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10